RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10 575,626
Source: IFWP
Date Processed by STIC: 3/20/07

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10575,626

CRF Edit Date: 3/20/07

Edited by: TCC

_____ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

_____ Corrected the SEQ ID NO. Sequence numbers edited were:

_____

_____ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

_____

✓ Deleted:___ invalid beginning/end-of-file text ; ___ page numbers

_____ Inserted mandatory headings/numeric identifiers, specifically:

_____

_____ Moved responses to same line as heading/numeric identifier, specifically:

_____

_____ Other:

_____
_____
_____

Revised 09/09/2003

IFWP

```
          3 <110> APPLICANT: Teijin Pharma Limited
W-->      4 <120> TITLE OF INVENTION: New Secretory Protein
W-->      5 <130> FILE REFERENCE: SAP-715-PCT
C-->      6 <140> CURRENT APPLICATION NUMBER: US/10/575,626
C-->      6 <141> CURRENT FILING DATE: 2006-04-13
W-->      6 <160> NUMBER OF SEQ ID: 9
          8 <170> SOFTWARE: PatentIn version 3.1
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         11 <211> LENGTH: 978
         12 <212> TYPE: DNA
         13 <213> ORGANISM: human.
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         16 <221> NAME/KEY: CDS
         17 <222> LOCATION: (1)..(951)
         18 <223> OTHER INFORMATION:
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     23 1               5                   10                  15
     25 gca gaa gct ttt aaa tcc aag aaa ata tgt aaa tca ctt aag att tgt      96
     26 Ala Glu Ala Phe Lys Ser Lys Lys Ile Cys Lys Ser Leu Lys Ile Cys
     27             20                  25                  30
     29 gga ctg gtg ttt ggt atc ctg gcc cta act cta att gtc ctg ttt tgg     144
     30 Gly Leu Val Phe Gly Ile Leu Ala Leu Thr Leu Ile Val Leu Phe Trp
     31         35              .       40          .       45
     33 ggg agc aag cac ttc tgg ccg gag gta ccc aaa aaa gcc tat gac atg     192
     34 Gly Ser Lys His Phe Trp Pro Glu Val Pro Lys Lys Ala Tyr Asp Met
     35         50                  55                  60
     37 gag cac act ttc tac agc aat gga gag aag aag aag att tac atg gaa     240
     38 Glu His Thr Phe Tyr Ser Asn Gly Glu Lys Lys Lys Ile Tyr Met Glu
     39 65                  70                  75                  80
     41 att gat cct gtg acc aga act gaa ata ttc aga agc gga aat ggc act     288
     42 Ile Asp Pro Val Thr Arg Thr Glu Ile Phe Arg Ser Gly Asn Gly Thr
     43                 85                  90                  95
     45 gat gaa aca ttg gaa gta cac gac ttt aaa aac gga tac act ggc atc     336
     46 Asp Glu Thr Leu Glu Val His Asp Phe Lys Asn Gly Tyr Thr Gly Ile
     47                 100                 105                 110
     49 tac ttc gtg ggt ctt caa aaa tgt ttt atc aaa act cag att aaa gtg     384
     50 Tyr Phe Val Gly Leu Gln Lys Cys Phe Ile Lys Thr Gln Ile Lys Val
     51         115                 120                 125
     53 att cct gaa ttt tct gaa cca gaa gag gaa ata gat gag aat gaa gaa     432
     54 Ile Pro Glu Phe Ser Glu Pro Glu Glu Glu Ile Asp Glu Asn Glu Glu
     55         130                 135                 140
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RAW SEQUENCE LISTING

DATE: 03/20/2007

PATENT APPLICATION: US/10/575,626

TIME: 17:48:53

Input Set : A:\pto.kd.txt
Output Set: N:\CRF4\03202007\J575626.raw

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57 att acc aca act ttc ttt gaa cag tca gtg att tgg gtc cca gca gaa        480
58 Ile Thr Thr Thr Phe Phe Glu Gln Ser Val Ile Trp Val Pro Ala Glu
59 145             150             155             160
61 aag cct att gaa aac cga gat ttt ctt aaa aat tcc aaa att ctg gag        528
62 Lys Pro Ile Glu Asn Arg Asp Phe Leu Lys Asn Ser Lys Ile Leu Glu
63             165             170             175
65 att tgt gat aac gtg acc atg tat tgg atc aat ccc act cta ata tca        576
66 Ile Cys Asp Asn Val Thr Met Tyr Trp Ile Asn Pro Thr Leu Ile Ser
67             180             185             190
69 gtt tct gag tta caa gac ttt gag gag gag gga gaa gat ctt cac ttt        624
70 Val Ser Glu Leu Gln Asp Phe Glu Glu Glu Gly Glu Asp Leu His Phe
71             195             200             205
73 cct gcc aac gaa aaa aaa ggg att gaa caa aat gaa cag tgg gtg gtc        672
74 Pro Ala Asn Glu Lys Lys Gly Ile Glu Gln Asn Glu Gln Trp Val Val
75     210             215             220
77 cct caa gtg aaa gta gag aag acc cgt cac gcc aga caa gca agt gag        720
78 Pro Gln Val Lys Val Glu Lys Thr Arg His Ala Arg Gln Ala Ser Glu
79 225             230             235             240
81 gaa gaa ctt cca ata aat gac tat act gaa aat gga ata gaa ttt gat        768
82 Glu Glu Leu Pro Ile Asn Asp Tyr Thr Glu Asn Gly Ile Glu Phe Asp
83             245             250             255
85 ccc atg ctg gat gag aga ggt tat tgt tgt att tac tgc cgt cga ggc        816
86 Pro Met Leu Asp Glu Arg Gly Tyr Cys Cys Ile Tyr Cys Arg Arg Gly
87             260             265             270
89 aac cgc tat tgc cgc cgc gtc tgt gaa cct tta cta ggc tac tac cca        864
90 Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly Tyr Tyr Pro
91     275             280             285
93 tat cca tac tgc tac caa gga gga cga gtc atc tgt cgt gtc atc atg        912
94 Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys Arg Val Ile Met
95     290             295             300
97 cct tgt aac tgg tgg gtg gcc cgc atg ctg ggg agg gtc gactacaaag        961
98 Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly Arg Val
99 305             310             315
101 acgatgacga caagtga                                                     978
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105 <211> LENGTH: 317
106 <212> TYPE: PRT
107 <213> ORGANISM: human
109 <400> SEQUENCE: 2
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114 Ala Glu Ala Phe Lys Ser Lys Lys Ile Cys Lys Ser Leu Lys Ile Cys
115             20             25             30
117 Gly Leu Val Phe Gly Ile Leu Ala Leu Thr Leu Ile Val Leu Phe Trp
118             35             40             45
120 Gly Ser Lys His Phe Trp Pro Glu Val Pro Lys Lys Ala Tyr Asp Met
121     50             55             60
123 Glu His Thr Phe Tyr Ser Asn Gly Glu Lys Lys Lys Ile Tyr Met Glu
124 65             70             75             80
```

```
126 Ile Asp Pro Val Thr Arg Thr Glu Ile Phe Arg Ser Gly Asn Gly Thr
127              85                  90                  95
129 Asp Glu Thr Leu Glu Val His Asp Phe Lys Asn Gly Tyr Thr Gly Ile
130             100                 105                 110
132 Tyr Phe Val Gly Leu Gln Lys Cys Phe Ile Lys Thr Gln Ile Lys Val
133         115                 120                 125
135 Ile Pro Glu Phe Ser Glu Pro Glu Glu Glu Ile Asp Glu Asn Glu Glu
136     130                 135                 140
138 Ile Thr Thr Thr Phe Phe Glu Gln Ser Val Ile Trp Val Pro Ala Glu
139 145                 150                 155                 160
141 Lys Pro Ile Glu Asn Arg Asp Phe Leu Lys Asn Ser Lys Ile Leu Glu
142             165                 170                 175
144 Ile Cys Asp Asn Val Thr Met Tyr Trp Ile Asn Pro Thr Leu Ile Ser
145             180                 185                 190
147 Val Ser Glu Leu Gln Asp Phe Glu Glu Glu Gly Glu Asp Leu His Phe
148         195                 200                 205
150 Pro Ala Asn Glu Lys Lys Gly Ile Glu Gln Asn Glu Gln Trp Val Val
151     210                 215                 220
153 Pro Gln Val Lys Val Glu Lys Thr Arg His Ala Arg Gln Ala Ser Glu
154 225                 230                 235                 240
156 Glu Glu Leu Pro Ile Asn Asp Tyr Thr Glu Asn Gly Ile Glu Phe Asp
157             245                 250                 255
159 Pro Met Leu Asp Glu Arg Gly Tyr Cys Cys Ile Tyr Cys Arg Arg Gly
160             260                 265                 270
162 Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly Tyr Tyr Pro
163         275                 280                 285
165 Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys Arg Val Ile Met
166     290                 295                 300
168 Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly Arg Val
169 305                 310                 315
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174 <212> TYPE: DNA
175 <213> ORGANISM: human
177 <220> FEATURE:
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179 <222> LOCATION: (1)..(246)
180 <223> OTHER INFORMATION:
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185 1               5                   10                  15
187 ata gaa ttt gat ccc atg ctg gat gag aga ggt tat tgt tgt att tac      96
188 Ile Glu Phe Asp Pro Met Leu Asp Glu Arg Gly Tyr Cys Cys Ile Tyr
189             20                  25                  30
191 tgc cgt cga ggc aac cgc tat tgc cgc cgc gtc tgt gaa cct tta cta      144
192 Cys Arg Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu
193         35                  40                  45
195 ggc tac tac cca tat cca tac tgc tac caa gga gga cga gtc atc tgt      192
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W--> 182

RAW SEQUENCE LISTING DATE: 03/20/2007
PATENT APPLICATION: US/10/575,626 TIME: 17:48:53

Input Set : A:\pto.kd.txt
Output Set: N:\CRF4\03202007\J575626.raw

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196 Gly Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys
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199 cgt gtc atc atg cct tgt aac tgg tgg gtg gcc cgc atg ctg ggg agg    240
200 Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly Arg
201 65              70              75              80
203 gtc taa                                                            246
204 Val
208 <210> SEQ ID NO: 4
209 <211> LENGTH: 81
210 <212> TYPE: PRT
211 <213> ORGANISM: human
213 <400> SEQUENCE: 4
215 Gln Ala Ser Glu Glu Glu Leu Pro Ile Asn Asp Tyr Thr Glu Asn Gly
216 1               5               10              15
218 Ile Glu Phe Asp Pro Met Leu Asp Glu Arg Gly Tyr Cys Cys Ile Tyr
219             20              25              30
221 Cys Arg Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu
222         35              40              45
224 Gly Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys
225     50              55              60
227 Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly Arg
228 65              70              75              80
230 Val
233 <210> SEQ ID NO: 5
234 <211> LENGTH: 303
235 <212> TYPE: DNA
236 <213> ORGANISM: human
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240 <222> LOCATION: (1)..(303)
241 <223> OTHER INFORMATION:
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246 1               5               10              15
248 aag tcg cga caa gca agt gag gaa gaa ctt cca ata aat gac tat act    96
249 Lys Ser Arg Gln Ala Ser Glu Glu Glu Leu Pro Ile Asn Asp Tyr Thr
250             20              25              30
252 gaa aat gga ata gaa ttt gat ccc atg ctg gat gag aga ggt tat tgt    144
253 Glu Asn Gly Ile Glu Phe Asp Pro Met Leu Asp Glu Arg Gly Tyr Cys
254         35              40              45
256 tgt att tac tgc cgt cga ggc aac cgc tat tgc cgc cgc gtc tgt gaa    192
257 Cys Ile Tyr Cys Arg Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu
258     50              55              60
260 cct tta cta ggc tac tac cca tat cca tac tgc tac caa gga gga cga    240
261 Pro Leu Leu Gly Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg
262 65              70              75              80
264 gtc atc tgt cgt gtc atc atg cct tgt aac tgg tgg gtg gcc cgc atg    288
265 Val Ile Cys Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met
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266                    85              90                   95
268 ctg ggg agg gtc taa                                               303
269 Leu Gly Arg Val
270                    100
273 <210> SEQ ID NO: 6
274 <211> LENGTH: 100
275 <212> TYPE: PRT
276 <213> ORGANISM: human
278 <400> SEQUENCE: 6
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281 1                   5                10                  15
283 Lys Ser Arg Gln Ala Ser Glu Glu Glu Leu Pro Ile Asn Asp Tyr Thr
284                    20               25                  30
286 Glu Asn Gly Ile Glu Phe Asp Pro Met Leu Asp Glu Arg Gly Tyr Cys
287              35             40                   45
289 Cys Ile Tyr Cys Arg Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu
290       50                  55                  60
292 Pro Leu Leu Gly Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg
293 65                  70                  75                  80
295 Val Ile Cys Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met
296                    85               90                   95
298 Leu Gly Arg Val
299                    100
302 <210> SEQ ID NO: 7
303 <211> LENGTH: 420
304 <212> TYPE: DNA
305 <213> ORGANISM: human
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308 <221> NAME/KEY: CDS
309 <222> LOCATION: (1)..(420)
310 <223> OTHER INFORMATION:
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315 1                   5                10                  15
317 aag tcg cga gaa gtg gta aga aaa att gtt cca act acc aca aaa aga     96
318 Lys Ser Arg Glu Val Val Arg Lys Ile Val Pro Thr Thr Thr Lys Arg
319                    20               25                  30
321 cca cac agt gga cca cgg agc aac cca ggc gct gga aga ctg aat aat    144
322 Pro His Ser Gly Pro Arg Ser Asn Pro Gly Ala Gly Arg Leu Asn Asn
323              35             40                   45
325 gaa acc aga ccc agt gtt caa gag gac tca caa gcc ttc aat cct gat    192
326 Glu Thr Arg Pro Ser Val Gln Glu Asp Ser Gln Ala Phe Asn Pro Asp
327       50                  55                  60
329 aat cct tat cat cag cag gaa ggg gaa agc atg aca ttc gac cct aga    240
330 Asn Pro Tyr His Gln Gln Glu Gly Glu Ser Met Thr Phe Asp Pro Arg
331 65                  70                  75                  80
333 ctg gat cac gaa gga atc tgt tgt ata gaa tgt agg cgg agc tac acc    288
334 Leu Asp His Glu Gly Ile Cys Cys Ile Glu Cys Arg Arg Ser Tyr Thr
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VERIFICATION SUMMARY   DATE: 03/20/2007
PATENT APPLICATION: **US/10/575,626**   TIME: 17:48:54

Input Set : **A:\pto.kd.txt**
Output Set: **N:\CRF4\03202007\J575626.raw**

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L:4 M:283 W: Missing Blank Line separator, <120> field identifier
L:5 M:283 W: Missing Blank Line separator, <130> field identifier
L:6 M:270 C: Current Application Number differs, Replaced Current Application No
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:6 M:283 W: Missing Blank Line separator, <160> field identifier
L:20 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:18
L:182 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:180
L:243 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:241
L:312 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:310
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Raw Sequence Listing before editing (for reference only)

IFWP

RAW SEQUENCE LISTING   DATE: 03/15/2007
PATENT APPLICATION: US/10/575,626   TIME: 11:02:43

Input Set : A:\PTO.SS.txt
Output Set: N:\CRF4\03152007\J575626.raw

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W-->  5 <130> FILE REFERENCE: SAP-715-PCT
C-->  6 <140> CURRENT APPLICATION NUMBER: US/10/575,626
C-->  6 <141> CURRENT FILING DATE: 2006-04-13
W-->  6 <160> NUMBER OF SEQ ID: 9
      8 <170> SOFTWARE: PatentIn version 3.1
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Does Not Comply
Corrected Diskette Needed
(PJ.1)

ERRORED SEQUENCES

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    387 <212> TYPE: PRT
    388 <213> ORGANISM: human
    390 <400> SEQUENCE: 9
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    393 1                   5                   10                  15
    395 Glu Phe Asp Pro Met Leu Asp Glu Arg Gly Tyr Cys Cys Ile Tyr Cys
    396             20                  25                  30
    398 Arg Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly
    399         35                  40                  45
    401 Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys Arg
    402     50                  55                  60
    404 Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly Arg Val
    405 65                  70                  75                  80
E-->408 14
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deleted

VERIFICATION SUMMARY   DATE: 03/15/2007
PATENT APPLICATION: US/10/575,626   TIME: 11:02:44

Input Set : **A:\PTO.SS.txt**
Output Set: **N:\CRF4\03152007\J575626.raw**

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L:5 M:283 W: Missing Blank Line separator, <130> field identifier
L:6 M:270 C: Current Application Number differs, Replaced Current Application No
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:6 M:283 W: Missing Blank Line separator, <160> field identifier
L:20 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:18
L:182 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:180
L:243 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:241
L:312 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:310
L:408 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
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